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RAW SEQUENCE LISTING

DATE: 03/06/2002

PATENT APPLICATION: US/09/960,428

TIME: 12:56:31

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF3\03062002\I960428.raw

3 <110> APPLICANT: Roche Diagnostics GmbH
 5 <120> TITLE OF INVENTION: Method for producing an active heterodimeric AMV-RT in prokaryotic cells
 7 <130> FILE REFERENCE: 5272/00/
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/960,428
 C--> 10 <141> CURRENT FILING DATE: 2001-09-21
 12 <160> NUMBER OF SEQ ID NOS: 22
 14 <170> SOFTWARE: PatentIn Ver. 2.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 38
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Artificial Sequence
 21 <220> FEATURE:
 22 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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 29 <212> TYPE: DNA
 30 <213> ORGANISM: Artificial Sequence
 32 <220> FEATURE:
 33 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 35 <400> SEQUENCE: 2
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 38 <210> SEQ ID NO: 3
 39 <211> LENGTH: 41
 40 <212> TYPE: DNA
 41 <213> ORGANISM: Artificial Sequence
 43 <220> FEATURE:
 44 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 46 <400> SEQUENCE: 3
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 49 <210> SEQ ID NO: 4
 50 <211> LENGTH: 171
 51 <212> TYPE: DNA
 52 <213> ORGANISM: Avian Myeloblastosis Virus
 54 <400> SEQUENCE: 4
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 57 gaattacagt taggacatat agaacccttca cttagtgtgt ggaacacac tgtctttgtg 180
 58 atccgggaagg ctcccggtc ttatcgctta ttgcctgaact tgcgcgtgt taaagctaa 240
 59 ctgtttctct ttggggcgt ccaacaggg gcgcgggtt cctccgcgt ccgcgtggc 300
 60 tggccctga tggctcaga cctcaaggat tgcttcttt ctattctct tgcggaacaa 360
 61 gatcgcggaag cttttgatt taagctccc totgtgaata accagggccc cgtctgaaga 420

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63 gtgggtcaaa tacttgagcc cttggagactc aagcaccat ctctggccat gttgcattat 540
64 atggatgata ttttgctagc cgcctcaagt catgatgggt tggaaagcgc aggggaggag 600
65 gttatcagta cattggaaa agcgggggttc accatttgc ctgataaggt ccagagggag 660
66 ccgggagtag aatatcttgg gtacaagtta ggcagtagct atgtagcacc cgtaggcctg 720
67 gtagcagaac ccaggatagc cactttgttg gatgttcaga agctgggtgg gtcacttcag 780
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69 ccaggggtcag atcctaacga ggcgagggaa tggaaatctag acatgaaaat ggccctggaga 900
70 agatcgtgc agctcagcac cactgctgcc ttggaacgat gggaccctgc cctgcctctg 960
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72 acacacccaa ggcctgttt gtggttattc tccacccaac ccaccaaggc gtttactgct 1080
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86 <211> LENGTH: 2574
87 <212> TYPE: DNA
88 <213> ORGANISM: Avian Myeloblastosis Virus
89 <400> SEQUENCE: 5
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93 gaattacagt taggacatat agaaccttca cttagtgtct ggaacacacc tgtctttgtg 180
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113 cctgtaccgg gacccactgt ctttaccgac gectectcaa gcacccataa ggggttggtta 1380
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115 caacaactgg aagcaacggc tgtggccatg gcacttctgc tgtggccgac aacgcccact 1500
116 aatgtagtga ctgactctgc gtttggttgcg aaaatgttac tcaagatggg gcagtagggga 1560
117 gtcccgctta cagcgggggc ttttatitta gaggatgcgt taagccaaag gtccagccatg 1620
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132 gtgaaaaaca gggacactga taaggttatt tgggtacct ctgaaaaagt taaacgggac 2520
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135 <210> SEQ ID NO: 6

136 <211> LENGTH: 572

137 <212> TYPE: PR

138 <213> ORGANISM: Avian Myeloblastosis Virus

140 <400> SEQUENCE: 6

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142 1 5 10 15
144 Thr Pro Val Trp Ile Asp Gln Trp Pro Leu Pro Glu Gly Lys Leu Val
145 20 25 30
147 Ala Leu Thr Gln Leu Val Glu Lys Glu Leu Gln Leu Gly His Ile Glu
148 35 40 45
150 Pro Ser Leu Ser Cys Trp Asn Thr Pro Val Phe Val Ile Arg Lys Ala
151 50 55 60
153 Ser Gly Ser Tyr Arg Leu Leu His Asp Leu Arg Ala Val Asn Ala Lys
154 65 70 75 80
156 Leu Val Pro Phe Gly Ala Val Gln Gln Gly Ala Pro Val Leu Ser Ala
157 85 90 95
159 Leu Pro Arg Gly Trp Pro Leu Met Val Leu Asp Leu Lys Asp Cys Phe
160 100 105 110
162 Phe Ser Ile Pro Leu Ala Glu Gln Asp Arg Glu Ala Phe Ala Phe Thr
163 115 120 125
165 Leu Pro Ser Val Asn Asn Gln Ala Pro Ala Arg Arg Phe Gln Trp Lys
166 130 135 140
168 Val Leu Pro Gln Gly Met Thr Cys Ser Pro Thr Ile Cys Gln Leu Ile
169 145 150 155 160
171 Val Gly Gln Ile Leu Glu Pro Leu Arg Leu Lys His Pro Ser Leu Arg
172 165 170 175
174 Met Leu His Tyr Met Asp Asp Leu Leu Leu Ala Ala Ser Ser His Asp

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175          180          185          190
177 Gly Leu Glu Ala Ala Gly Glu Glu Val Ile Ser Thr Leu Glu Arg Ala
178          195          200          205
180 Gly Phe Thr Ile Ser Pro Asp Lys Val Gln Arg Glu Pro Gly Val Gln
181          210          215          220
183 Tyr Leu Gly Tyr Lys Leu Gly Ser Thr Tyr Val Ala Pro Val Gly Leu
184 225          230          235          240
186 Val Ala Glu Pro Arg Ile Ala Thr Leu Trp Asp Val Gln Lys Leu Val
187          245          250          255
189 Gly Ser Leu Gln Trp Leu Arg Pro Ala Leu Gly Ile Pro Pro Arg Leu
190          260          265          270
192 Met Gly Pro Phe Tyr Glu Gln Leu Arg Gly Ser Asp Pro Asn Glu Ala
193          275          280          285
195 Arg Glu Trp Asn Leu Asp Met Lys Met Ala Trp Arg Glu Ile Val Gln
196          290          295          300
198 Leu Ser Thr Thr Ala Ala Leu Glu Arg Trp Asp Pro Ala Leu Pro Leu
199 305          310          315          320
201 Glu Gly Ala Val Ala Arg Cys Glu Gln Gly Ala Ile Gly Val Leu Gly
202          325          330          335
204 Gln Gly Leu Ser Thr His Pro Arg Pro Cys Leu Trp Leu Phe Ser Thr
205          340          345          350
207 Gln Pro Thr Lys Ala Phe Thr Ala Trp Leu Glu Val Leu Thr Leu Leu
208          355          360          365
210 Ile Thr Lys Leu Arg Ala Ser Ala Val Arg Thr Phe Gly Lys Glu Val
211          370          375          380
213 Asp Ile Leu Leu Leu Pro Ala Cys Phe Arg Glu Asp Leu Pro Leu Pro
214 385          390          395          400
216 Glu Gly Ile Leu Leu Ala Leu Arg Gly Phe Ala Gly Lys Ile Arg Ser
217          405          410          415
219 Ser Asp Thr Pro Ser Ile Phe Asp Ile Ala Arg Pro Leu His Val Ser
220          420          425          430
222 Leu Lys Val Arg Val Thr Asp His Pro Val Pro Gly Pro Thr Val Phe
223          435          440          445
225 Thr Asp Ala Ser Ser Ser Thr His Lys Gly Val Val Val Trp Arg Glu
226          450          455          460
228 Gly Pro Arg Trp Glu Ile Lys Glu Ile Ala Asp Leu Gly Ala Ser Val
229 465          470          475          480
231 Gln Gln Leu Glu Ala Arg Ala Val Ala Met Ala Leu Leu Leu Trp Pro
232          485          490          495
234 Thr Thr Pro Thr Asn Val Val Thr Asp Ser Ala Phe Val Ala Lys Met
235          500          505          510
237 Leu Leu Lys Met Gly Gln Glu Gly Val Pro Ser Thr Ala Ala Ala Phe
238          515          520          525
240 Ile Leu Glu Asp Ala Leu Ser Gln Arg Ser Ala Met Ala Ala Val Leu
241          530          535          540
243 His Val Arg Ser His Ser Glu Val Pro Gly Phe Phe Thr Glu Gly Asn
244 545          550          555          560
246 Asp Val Ala Asp Ser Gln Ala Thr Phe Gln Ala Tyr
247          565          570

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249 <210> SEQ ID NO: 7
250 <211> LENGTH: 858
251 <212> TYPE: PRT
252 <213> ORGANISM: Avian Myeloblastosis Virus
254 <400> SEQUENCE: 7
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259      20              25              30
261 Ala Leu Thr Gln Leu Val Glu Lys Glu Leu Gln Leu Gly His Ile Glu
262      35              40              45
264 Pro Ser Leu Ser Cys Trp Asn Thr Pro Val Phe Val Ile Arg Lys Ala
265      50              55              60
267 Ser Gly Ser Tyr Arg Leu Leu His Asp Leu Arg Ala Val Asn Ala Lys
268      65              70              75              80
270 Leu Val Pro Phe Gly Ala Val Gln Gln Gly Ala Pro Val Leu Ser Ala
271      85              90              95
273 Leu Pro Arg Gly Trp Pro Leu Met Val Leu Asp Leu Lys Asp Cys Phe
274      100             105             110
276 Phe Ser Ile Pro Leu Ala Glu Gln Asp Arg Glu Ala Phe Ala Phe Thr
277      115             120             125
279 Leu Pro Ser Val Asn Asn Gln Ala Pro Ala Arg Arg Phe Gln Trp Lys
280      130             135             140
282 Val Leu Pro Gln Gly Met Thr Cys Ser Pro Thr Ile Cys Gln Leu Ile
283      145             150             155             160
285 Val Gly Gln Ile Leu Glu Pro Leu Arg Leu Lys His Pro Ser Leu Arg
286      165             170             175
288 Met Leu His Tyr Met Asp Asp Leu Leu Ala Ala Ser Ser His Asp
289      180             185             190
291 Gly Leu Glu Ala Ala Gly Glu Glu Val Ile Ser Thr Leu Glu Arg Ala
292      195             200             205
294 Gly Phe Thr Ile Ser Pro Asp Lys Val Gln Arg Glu Pro Gly Val Gln
295      210             215             220
297 Tyr Leu Gly Tyr Lys Leu Gly Ser Thr Tyr Val Ala Pro Val Gly Leu
298      225             230             235             240
300 Val Ala Glu Pro Arg Ile Ala Thr Leu Trp Asp Val Gln Lys Leu Val
301      245             250             255
303 Gly Ser Leu Gln Trp Leu Arg Pro Ala Leu Gly Ile Pro Pro Arg Leu
304      260             265             270
306 Met Gly Pro Phe Tyr Glu Gln Leu Arg Gly Ser Asp Pro Asn Glu Ala
307      275             280             285
309 Arg Glu Trp Asn Leu Asp Met Lys Met Ala Trp Arg Glu Ile Val Gln
310      290             295             300
312 Leu Ser Thr Thr Ala Ala Leu Glu Arg Trp Asp Pro Ala Leu Pro Leu
313      305             310             315             320
315 Glu Gly Ala Val Ala Arg Cys Glu Gln Gly Ala Ile Gly Val Leu Gly
316      325             330             335
318 Gln Gly Leu Ser Thr His Pro Arg Pro Cys Leu Trp Leu Phe Ser Thr
319      340             345             350

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VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date